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SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-73

10 <140> PCT/CA99/01230

<141> 1999-12-23

<150> 60/113,280

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 Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg Glu Ser Lys Leu Phe
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Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg Ile Gly Glu Ala Phe
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 Met Arg Phe Ser Leu
 1 5

30 tgc gga ttt cct cta gtt ttt tct ttt aca ttg ctc tca gtc ttc gac 163
 Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu Leu Ser Val Phe Asp
 10 15 20

act tct ttg agt gct act acg att tct tta acc cca gaa gat agt ttt 211
 Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr Pro Glu Asp Ser Phe
 25 30 35

cat gga gat agt cag aat gca gaa cgt tct tat aat gtt caa gct ggg 259
 His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr Asn Val Gln Ala Gly
 40 45 50

40 gat gtc tat agc ctt act ggt gat gtc tca ata tct aac gtc gat aac 307
 Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile Ser Asn Val Asp Asn
 55 60 65

tct gca tta aat aaa gcc tgc ttc aat gtg acc tca gga agt gtg acg 355
 Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr Ser Gly Ser Val Thr
 70 75 80 85

50 ttc gca gga aat cat cat ggg tta tat ttt aat aat att tcc tca gga 403
 Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn Asn Ile Ser Ser Gly
 90 95 100

act aca aag gaa ggg gct gta ctt tgt tgc caa gat cct caa gca acg 451
 Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln Asp Pro Gln Ala Thr
 105 110 115

gca cgt ttt tct ggg ttc tcc acg ctc tct ttt att cag agc ccc gga 499
 Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe Ile Gln Ser Pro Gly
 120 125 130

gat att aaa gaa cag gga tgt ctc tat tca aaa aat gca ctt atg ctc 547
 Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys Asn Ala Leu Met Leu
 135 140 145

tta aac aat tat gta gtg cgt ttt gaa caa aac caa agt aag act aaa 595
 Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn Gln Ser Lys Thr Lys
 150 155 160 165

10 ggc gga gct att agt ggg gcg aat gtt act ata gta ggc aac tac gat 643
 Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile Val Gly Asn Tyr Asp
 170 175 180

tcc gtc tct ttc tat cag aat gca gcc act ttt gga ggt gct atc cat 691
 Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe Gly Gly Ala Ile His
 185 190 195

tct tca ggt ccc cta cag att gca gta aat cag gca gag ata aga ttt 739
 Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln Ala Glu Ile Arg Phe
 200 205 210

20 gca caa aat act gcc aag aat ggt tct gga ggg gct ttg tac tcc gat 787
 Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly Ala Leu Tyr Ser Asp
 215 220 225

ggt gat att gat att gat cag aat gct tat gtt cta ttt cga gaa aat 835
 Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val Leu Phe Arg Glu Asn
 230 235 240 245

30 gag gca ttg act act gct ata ggt aag gga ggg gct gtc tgt tgt ctt 883
 Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly Ala Val Cys Cys Leu
 250 255 260

ccc act tca gga agt agt act cca gtt cct att gtg act ttc tct gac 931
 Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile Val Thr Phe Ser Asp
 265 270 275

aat aaa cag tta gtc ttt gaa aga aac cat tcc ata atg ggt ggc gga 979
 Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser Ile Met Gly Gly Gly
 280 285 290

40 gcc att tat gct agg aaa ctt agc atc tct tca gga ggt cct act cta 1027
 Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser Gly Gly Pro Thr Leu
 295 300 305

ttt atc aat aat ata tca tat gca aat tcg caa aat tta ggt gga gct 1075
 Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln Asn Leu Gly Gly Ala
 310 315 320 325

50 att gcc att gat act gga ggg gag atc agt tta tca gca gag aaa gga 1123
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 330 335 340

aca att aca ttc caa gga aac cgg acg agc tta ccg ttt ttg aat ggc 1171
 Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu Pro Phe Leu Asn Gly
 345 350 355

atc cat ctt tta caa aat gct aaa ttc ctg aaa tta cag gcg aga aat 1219
 Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys Leu Gln Ala Arg Asn
 360 365 370

gga tac tct ata gaa ttt tat gat cct att act tct gaa gca gat ggg 1267
 Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr Ser Glu Ala Asp Gly
 375 380 385

10 tct acc caa ttg aat atc aac gga gat cct aaa aat aaa gag tac aca 1315
 Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys Asn Lys Glu Tyr Thr
 390 395 400 405

ggg acc ata ctc ttt tct gga gaa aag agt cta gca aac gat cct agg 1363
 Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg
 410 415 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac 1411
 Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr
 425 430 435

20 tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag 1459
 Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val Ser Lys Phe Thr Gln
 440 445 450

B tct cca gga tcg cat tta gtt tta gat tta gga acc aaa ctg ata gcc 1507
 Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala
 455 460 465

30 tct aag gaa gac att gcc atc aca ggc ctc gcg ata gat ata gat agc 1555
 Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala Ile Asp Ile Asp Ser
 470 475 480 485

tta agc tca tcc tca aca gca gct gtt att aaa gca aac acc gca aat 1603
 Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys Ala Asn Thr Ala Asn
 490 495 500

aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc 1651
 Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu Ile Ser Pro Thr Gly
 505 510 515

40 aat gcc tat gaa gat ctc aga atg aga aat tca cag acg ttc cct ctg 1699
 Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser Gln Thr Phe Pro Leu
 520 525 530

ctc tct tta gag cct gga gcc ggg ggt agt gtg act gta act gct gga 1747
 Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val Thr Val Thr Ala Gly
 535 540 545

gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa 1795
 Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe Gln Gly Asn Trp Lys
 550 555 560 565

50 tta gct tgg aca gga act gga aac aaa gtt gga gaa ttc ttc tgg gat 1843
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 570 575 580

aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct 1891
 Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro
 585 590 595

aat atc ttg tgg ggg aat gct gta gat gtc aga tcc tta atg cag gtt 1939
 Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val
 600 605 610

10 caa gag acc cat gca tcg agc tta cag aca gat cga ggg ctg tgg atc 1987
 Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile
 615 620 625

gat gga att ggg aat ttc ttc cat gta tct gcc tcc gaa gac aat ata 2035
 Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala Ser Glu Asp Asn Ile
 630 635 640 645

agg tac cgt cat aac agc ggt gga tat gtt cta tct gta aat aat gag 2083
 Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu Ser Val Asn Asn Glu
 650 655 660

20 atc aca cct aag cac tat act tcg atg gca ttt tcc caa ctc ttt agt 2131
 Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser
 665 670 675

aga gac aag gac tat gcg gtt tcc aac aac gaa tac aga atg tat tta 2179
 Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu Tyr Arg Met Tyr Leu
 680 685 690

30 gga tcg tat ctc tat caa tat aca acc tcc cta ggg aat att ttc cgt 2227
 Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu Gly Asn Ile Phe Arg
 695 700 705

tat gct tcg cgt aac cct aat gta aac gtc ggg att ctc tca aga agg 2275
 Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg
 710 715 720 725

ttt ctt caa aat cct ctt atg att ttt cat ttt ttg tgt gct tat ggt 2323
 Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe Leu Cys Ala Tyr Gly
 730 735 740

40 cat gcc acc aat gat atg aaa aca gac tac gca aat ttc cct atg gtg 2371
 His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val
 745 750 755

aaa aac agc tgg aga aac aat tgt tgg gct ata gag tgc gga ggg agc 2419
 Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser
 760 765 770

50 atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc 2467
 Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu Phe Gln Gly Ala Ile
 775 780 785

cca ttt atg aaa cta caa tta gtt tat gct tat cat gga gat ttc aaa 2515
 Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr His Gly Asp Phe Lys
 790 795 800 805

gag acg act gca gat ggc cgt aga ttt agt aat ggg agt tta aca tcg 2563
 Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn Gly Ser Leu Thr Ser
 810 815 820

att tct gta cct cta ggc ata cgc ttt gag aag ctg gca ctt tct cag 2611
 Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys Leu Ala Leu Ser Gln
 825 830 835

10 gat gta ctc tat gac ttt agt ttc tcc tat att cct gat att ttc cgt 2659
 Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile Pro Asp Ile Phe Arg
 840 845 850

aag gat ccc tca tgt gaa gct gct ctg gtg att agc gga gac tcc tgg 2707
 Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile Ser Gly Asp Ser Trp
 855 860 865

ctt gtt ccg gca gca cac gta tca aga cat gct ttt gta ggg agt gga 2755
 Leu Val Pro Ala Ala His Val Ser Arg His Ala Phe Val Gly Ser Gly
 870 875 880 885

20 acg ggt cgg tat cac ttt aac gac tat act gag ctc tta tgt cga gga 2803
 Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu Leu Leu Cys Arg Gly
 890 895 900

agt ata gaa tgc cgc ccc cat gct agg aat tat aat ata aac tgt gga 2851
 Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr Asn Ile Asn Cys Gly
 905 910 915

30 agc aaa ttt cgt ttt tagaagggtt ccattgcctg tgtgggttcg gatcttaact 2906
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40 <220>
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<220>
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 Met Pro Ser Ser Trp
 1 5

aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt 163
 Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser
 10 15 20

ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga 211
 Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly
 25 30 35

agc ttc aca att acc gat aat aaa gtc gaa act agt ctt act act agc 259
 Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser
 40 45 50

10 act aat tta tat ggt ggg ggc atc tat tcc agt gga gct gtc acg cta 307
 Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser Gly Ala Val Thr Leu
 55 60 65

acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat 355
 Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn
 70 75 80 85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca 403
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 90 95 100

20 acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc 451
 Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr Pro Ile Leu Phe Ser
 105 110 115

aac aac tct gct gcc act aaa aaa aca tca aca aca aag caa att gct 499
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 120 125 130

30 ggt ggg gct atc ttc tcc gct gca gta act atc gag aat aac tct cag 547
 Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile Glu Asn Asn Ser Gln
 135 140 145

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 Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala
 150 155 160 165

gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac 643
 Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn
 170 175 180

40 tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat 691
 Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr
 185 190 195

gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca 739
 Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser
 200 205 210

50 cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa 787
 Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln
 215 220 225

gac aac tct gcg tta aat cgc gga ggc gct atc tat gga gag act atc 835
 Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile Tyr Gly Glu Thr Ile
 230 235 240 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat 883
 Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly Asn Ser Ser Lys His
 250 255 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac 931
 Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn
 265 270 275

10 tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act 979
 Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr
 280 285 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat 1027
 Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn
 295 300 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att 1075
 Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile
 310 315 320 325

20 ttc ttt aaa aac aat cta tgc aca gca aca aac aaa tac tgc agt att 1123
 Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile
 330 335 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct 1171
 Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala
 345 350 355

30 ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc 1219
 Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu
 360 365 370

aag agc taaattaaat gaaaaagcga caagtacang gacgtttcta ntttctgggg 1275
 Lys Ser
 375

gacttcacgg aaataaatcc ctattccaca gaaagtcact tcgccctngg gat 1328

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 Met Lys Tyr Ser Leu
 1 5

cct tgg cta ctt acc tct tcg gct tta gtt ttc tcc cta cat cca cta 163
 Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe Ser Leu His Pro Leu
 10 15 20

atg gct gct aac acg gat ctc tca tca tcc gat aac tat gaa aat ggt 211
 Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp Asn Tyr Glu Asn Gly
 25 30 35

agt agt ggt agc gca gca ttc act gcc aag gaa act tcg gat gct tca 259
 Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu Thr Ser Asp Ala Ser
 40 45 50

10 gga act acc tac act ctc act agc gat gtt tct att acg aat gta tct 307
 Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser Ile Thr Asn Val Ser
 55 60 65

gca att act cct gca gat aaa agc tgt ttt aca aac aca gga gga gca 355
 Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr Asn Thr Gly Gly Ala
 70 75 80 85

ttg agt ttt gtt gga gct gat cac tca ttg gtt ctg caa acc ata gcg 403
 Leu Ser Phe Val Gly Ala Asp His Ser Leu Val Leu Gln Thr Ile Ala
 90 95 100

20 ctt acg cat gat ggt gct gca att aac aat acc aac aca gct ctt tct 451
 Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr Asn Thr Ala Leu Ser
 105 110 115

31 ttc tca gga ttc tcg tca ctc tta atc gac tca gct cca gca aca gga 499
 Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser Ala Pro Ala Thr Gly
 120 125 130

30 act tcg ggc ggc aag ggt gct att tgt gtg aca aat aca gag gga ggt 547
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 135 140 145

act gcg act ttt act gac aat gcc agt gtc acc ctc caa aaa aat act 595
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 150 155 160 165

tca gaa aaa gat gga gct gca gtt tct gcc tac agc atc gat ctt gct 643
 Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr Ser Ile Asp Leu Ala
 170 175 180

40 aag act acg aca gca gct ctc tta gat caa aat act agc aca aaa aat 691
 Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn Thr Ser Thr Lys Asn
 185 190 195

ggc ggg gcc ctc tgt agt aca gca aac act aca gtc caa gga aac tca 739
 Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr Val Gln Gly Asn Ser
 200 205 210

50 gga acg gtg acc ttc tcc tca aat act gct aca gat aaa ggt ggg ggg 787
 Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly
 215 220 225

atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc 835
 Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val
 230 235 240 245

gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct 883
 Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser
 250 255 260

gat gac aat ctt gct ctt acc ggc aac act caa gta ctt ttt cag gaa 931
 Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu
 265 270 275

10 aat aaa aca acc ggc tca gca gca cag gca aat aac ccg gaa ggt tgt 979
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 280 285 290

ggt ggg gca atc tgt tgt tat ctt gct aca gca aca gac aaa act gga 1027
 Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala Thr Asp Lys Thr Gly
 295 300 305

tta gcc att tct cag aat caa gaa atg agc ttc act agt aat aca aca 1075
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 310 315 320 325

20 act gcg aat ggt gga gcg atc tac gct act aaa tgt act ctg gat gga 1123
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 330 335 340

aac aca act ctt acc ttc gat cag aat act gcg aca gca gga tgt ggc 1171
 Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala Thr Ala Gly Cys Gly
 345 350 355

30 gga gct atc tat aca gaa act gaa gat ttt tct ctt aag gga agt acg 1219
 Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser Leu Lys Gly Ser Thr
 360 365 370

gga acc gtg acc ttc agc aca aat aca gca aag aca ggc ggc gcc tta 1267
 Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly Gly Ala Leu
 375 380 385

tat tct aaa gga aac agc tcg ctg act gga aat acc aac ctg ctc ttt 1315
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 390 395 400 405

40 tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca aat caa gag 1363
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 410 415 420

ggt tgc ggt ggg gca atc cta gcc ttt att gat tca gga tcc gta agc 1411
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 425 430 435

50 gat aaa aca gga cta tcg att gca aac aac caa gaa gtc agc ctc act 1459
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 440 445 450

agt aat gct gca aca gta agt ggt ggt gcg atc tat gct acc aaa tgt 1507
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 455 460 465

act cta act gga aac ggc tcc ctg acc ttt gac ggc aat act gct gga 1555
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 470 475 480 485

act tca gga ggg gcg atc tat aca gaa act gaa gat ttt act ctt aca 1603
 Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Thr Leu Thr
 490 495 500

10 gga agt aca gga acc gtg acc ttc agc aca aat aca gca aag aca ggc 1651
 Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly
 505 510 515

ggc gcc tta tat tct aaa ggc aac aac tct ctg tct ggt aat acc aac 1699
 Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu Ser Gly Asn Thr Asn
 520 525 530

ctg ctc ttt tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca 1747
 Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala
 535 540 545

20 aat caa gag ggt tgc ggt ggg gca atc cta tcg ttt ctt gag tca gca 1795
 Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Glu Ser Ala
 550 555 560 565

tct gta agt act aaa aaa gga ctc tgg att gaa gat aac gaa aac gtg 1843
 Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu Asp Asn Glu Asn Val
 570 575 580

30 agt ctc tct ggt aat act gca aca gta agt ggc ggt gcg atc tat gcg 1891
 Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala
 585 590 595

acc aag tgt gct ctg cat gga aac acg act ctt acc ttt gat ggc aat 1939
 Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn
 600 605 610

act gcc gaa act gca gga gga gcg atc tat aca gaa acc gaa gat ttt 1987
 Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe
 615 620 625

40 act ctt acg gga agt acg gga acc gtg acc ttc agc aca aat aca gca 2035
 Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala
 630 635 640 645

aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa 2083
 Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn Thr Ser Phe Thr Lys
 650 655 660

50 aat aag gct ctt gta ttt tct gga aat tca gca aca gca aca gca aca 2131
 Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala Thr Ala Thr Ala Thr
 665 670 675

aca act aca gat caa gaa ggt tgt ggt gga gcg atc ctc tgt aat atc 2179
 Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala Ile Leu Cys Asn Ile
 680 685 690

tca gag tct gac ata gct aca aaa agc tta act ctt act gaa aat gag 2227
 Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr Leu Thr Glu Asn Glu
 695 700 705

agt tta agt ttc att aac aat acg gca aaa aga agt ggt ggt ggt att 2275
 Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg Ser Gly Gly Gly Ile
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10 tat gct cct aag tgt gta atc tca ggc agt gaa tcc ata aac ttt gat 2323
 Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu Ser Ile Asn Phe Asp
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ggc aat act gct gaa act tcg gga gga gcg att tat tcg aaa aac ctt 2371
 Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile Tyr Ser Lys Asn Leu
 745 750 755

tcg att aca gct aac ggt cct gtc tcc ttt acc aat aat tct gga ggc 2419
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20 aag gga ggc gcc att tat ata gcc gat agc gga gaa ctt tcc tta gag 2467
 Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly Glu Leu Ser Leu Glu
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 Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn Arg Ala Thr Glu Gly
 790 795 800 805

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 Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr Phe Tyr Asp Pro Ile
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40 aat cct gtt gtc aaa gct att gtt cct cct ccc caa cca aaa aat ggt 2707
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cct ata tagaagaaaa acgaatgctc tttgtaaggc tcaagagtaa aaaattctaa 2763
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 Met Thr Asn Ser Ile
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10 ttc ata tca aag ttt gga tgt tta tgc gac cca ttt gtc tca gca ttt 163
 Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro Phe Val Ser Ala Phe
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tat ccc act gcg cta tgt tgt tcc tta tca gga aat gaa gtc cct aac 211
 Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly Asn Glu Val Pro Asn
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ctc gcc tct tgt cag atg tct aga aaa gac atc tct gct ttc cac acg 259
 Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His Thr
 40 45 50

20 tct cca agc ttc cgt ctg aat gta act cca gag ccc ttg gtt tcc tcc 307
 Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser Ser
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3 ttt cgt ccc tct aat ctt ctt aat gga ttc ggt cac gat ata acc cag 355
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30 gac atc aca att aca gga aac tct atc aat tct gtt ata gat tat aac 403
 Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr Asn
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tac cac tac gag gat gga ggc att ctt gca tgt aaa aat ttg ttc att 451
 Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys Lys Asn Leu Phe Ile
 105 110 115

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40 tct gga ggg gct ctc tac agt gtt cgg gaa tgc tgg att tct aag aat 547
 Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys Trp Ile Ser Lys Asn
 135 140 145

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 Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr Thr
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50 act tca gga ttt ggt ggg gct ata cat gca cta gat agc tat att aca 643
 Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr
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aat aac tta gga gaa gga caa ttc tta gat aat gtc tct aaa aat aga 691
 Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg
 185 190 195

gga gga gct atc tat gtt ggg gtg agt tta tca atc aca gac aac tta 739
 Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser Ile Thr Asp Asn Leu
 200 205 210

ggt cct atc gtt atc aag aaa aat caa aca tta gaa gat tcc agc ttt 787
 Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser Phe
 215 220 225

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 Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile Glu Arg Asn Tyr Gln
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10 aac atc caa atc aat gat aat gct tca gga caa ggg gtg gta tat ttt 883
 Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr Phe
 250 255 260

ctg ccc cta gga gtc att atc tct tca aat aaa gaa att ata gag atc 931
 Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys Glu Ile Ile Glu Ile
 265 270 275

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 Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala Ser Gly Lys Leu Tyr
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20 ccc ggt ggt ggc ggt atc atg tgt acc tcc ctt agt cat gag aac aat 1027
 Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu Ser His Glu Asn Asn
 295 300 305

ccc aaa ggt ctt atc ttt aac aat aaa acg gca gca ctt agc ggc gga 1075
 Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly
 310 315 320 325

30 gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca 1123
 Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile Thr Val Arg Thr Ala
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 Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser
 345 350 355

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40 gat att cta ttt aac aat aat aca atc aca tct tct tct cct caa ccc 1267
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 375 380 385

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50 gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac 1363
 Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His
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gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac 1411
 Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His
 425 430 435

ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca 1459
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aat cca ttg aac ttc cta tca aaa ttt tct aac tct tca cga ctt gaa 1507
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10 agg ggt gtg ctc gct att gaa gat cgg gct gct att tct tgc aaa acc 1555
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 470 475 480 485

cta tcg caa act ggg ggc att cta cgt tta gga aac gca gca tta atc 1603
 Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly Asn Ala Ala Leu Ile
 490 495 500

agg acg aaa ggc ccg gga agc tcc ata aat ttt aat gca atc gcg atc 1651
 Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile
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20 aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg 1699
 Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp
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 Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser
 535 540 545

act atc act ctc tca gga ccc ttg act ttt cta aac gat gaa aat gaa 1795
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 550 555 560 565

aac ccc tat gat agc tta gat ctc tct gaa cct cga aag gat atc ccc 1843
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 Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn
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40 ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga 1939
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atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca 1987
 Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Ser Ser Thr
 615 620 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg 2035
 Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln Leu Tyr Val Asp Trp
 630 635 640 645

50 act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att 2083
 Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg His Gly Glu Phe Ile
 650 655 660

gct aat acc tta tgg cag tct gcc tat aac gct ctg tta gga atc cgc 2131
 Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg
 665 670 675

atc tta cct cca caa aac ctc aaa gag cat gac ctt gaa gcc tct ctg 2179
 Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu
 680 685 690

10 caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa 2227
 Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn Arg Glu Gly Arg Lys
 695 700 705

ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa 2275
 Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys
 710 715 720 725

act gca gca cga cat agt ttc tct tta gga ttc gca caa atg ttc tcc 2323
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20 aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac 2371
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 760 765 770

aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc 2467
 Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys
 775 780 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac 2515
 His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn
 790 795 800 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc 2563
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 810 815 820

40 acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc 2611
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tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc 2659
 Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe
 840 845 850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt 2707
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 855 860 865

50 tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa 2755
 Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu
 870 875 880 885

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 890 895 900

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 905 910 915

10 tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc 2899
 Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe
 920 925 930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca 2947
 Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser
 935 940 945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt 2989
 Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His Cys Thr Phe
 950 955 960

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 Met Thr Ile Leu Arg
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40 aat ttt ctt acc tgc tcg gct tta ttc ctc gct ctc cct gca gca gca 163
 Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala
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caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat 211
 Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn
 25 30 35

aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct 259
 Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser
 40 45 50

50 tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa 307
 Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln
 55 60 65

gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg 355
 Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met
 70 75 80 85

ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt 403
 Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe
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 105 110 115

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 Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly
 120 125 130

caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag 547
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 135 140 145

20 gaa gtg act ttc tgt ggg aac tac tct tcg tgg agt gga gct gcg att 595
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 Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn
 170 175 180

ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt 691
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 185 190 195

30 tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga 739
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 200 205 210

cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat 787
 Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn
 215 220 225

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 230 235 240 245

40 aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga 883
 Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly
 250 255 260

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 Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys
 265 270 275

50 aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata 979
 Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile
 280 285 290

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 295 300 305

gaa gga aag gaa act tat gaa gga aca att agc ttc tca gga cta tgc 1075
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 310 315 320 325

ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta 1123
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 330 335 340

10 caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt 1171
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 345 350 355

acc ttg caa ctg cat tct ttt aag cag gaa gca agc tct acg ctt act 1219
 Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr
 360 365 370

atg tct cca gga acc act ctg ctc tgc tca gga gat gct cgg gtt cag 1267
 Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln
 375 380 385

20 aat ctg cac atc ctg att gaa gat acc gac aac ttt gtt cct gta agg 1315
 Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg
 390 395 400 405

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 410 415 420

30 gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag 1411
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 425 430 435

gaa gcc ttt acg att cct ctt ctt gaa ctt cta ggg cct tct ttt gac 1459
 Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp
 440 445 450

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 Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr
 455 460 465

40 gag aat gac gcc gtt cga ggt ttc tgg tcc cta agc tgg gaa gag tac 1555
 Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr
 470 475 480 485

ccc cct tct ctg gat aaa gac aga agg atc aca cca act aag aaa act 1603
 Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr
 490 495 500

50 gtt ttc ctc act tgg aat cct gag atc act tct acg cca taatctctaa 1652
 Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro
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<212> DNA

<213> Chlamydia pneumoniae

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<222> (101)..(967)

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 Met Gly Ile Ser Leu
 1 5

cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt 163
 Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe
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20 caa cat cct ccg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc 211
 Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Leu Ala
 25 30 35

cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag ctc 259
 Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu
 40 45 50

30 ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc 307
 Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile
 55 60 65

atc ttt cca aaa gtc ttg gcg gat acg cag atc aca aat tac atg gat 355
 Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp
 70 75 80 85

aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att 403
 Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu Met Ile Ile Gly Ile
 90 95 100

40 gtg ata ggc ttt gtt tta gca ttt ccc ttt tat gct gca caa tcg gca 451
 Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr Ala Ala Gln Ser Ala
 105 110 115

gga tct ttc atc act aac caa caa ggg att cag ggt tta gag ggc gcg 499
 Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln Gly Leu Glu Gly Ala
 120 125 130

aca tcc ctg att tcc att gag cag acc tct ccg cat ggc att tta tac 547
 Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro His Gly Ile Leu Tyr
 135 140 145

50 cat tac ttc gtg act att att ttt tgg tta gtg ggt ggt cac cgt att 595
 His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile
 150 155 160 165

gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt 643
 Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val Ile Pro Ile His Ser
 170 175 180

ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act 691
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 185 190 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt 739
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 200 205 210

10 gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att 787
 Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile
 215 220 225

att aac cgt atg gca cct caa gtt cag gtc atc tac ctc ctc tct gcc 835
 Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala
 230 235 240 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc 883
 Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe
 250 255 260

20 ata att aag cag ata gat tat ttc act ctt gct tgg ttc aaa gaa gtc 931
 Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val
 265 270 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatccccta 977
 Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val Leu
 280 285

30 ggctctttatc gtgactctta tctggagatg cgctcactta cgaatcttag cgcactggtt 1037
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 40 <222> (101)..(895)

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 Met Lys His Ser Lys
 1 5

50 gaa gat gac ctc tcc agg ttt ctt cct aaa aat ctt ctt gtt gaa tct 163
 Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu Leu Val Glu Ser
 10 15 20

cct cat ccc gaa gaa atc cct tta aaa tct tta tct ttt acg atg agt 211
 Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser Phe Thr Met Ser
 25 30 35

tgg cta cct aca att cat cct tca tgg att acc att gcc atg aaa gag 259
 Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile Ala Met Lys Glu
 40 45 50

ttc cct cct gaa atc caa ggt caa tta tta gcg tgg ttg cca gag cct 307
 Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp Leu Pro Glu Pro
 55 60 65

10 tta gtt caa gaa att cta ccc tta ctg cct ggc atc tct ata gcc cca 355
 Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile Ser Ile Ala Pro
 70 75 80 85

cat cgc tgt gca cct ttc gga gcc ttc tat ctt cta gat atg cta agt 403
 His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu Asp Met Leu Ser
 90 95 100

aaa aag atc cgt cct tgt gga att aca gaa gaa atc ttt ctt cct gca 451
 Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile Phe Leu Pro Ala
 105 110 115

20 tcc tca gca aat gct ata ctt tac tat aca ggt cct gta aag atc gct 499
 Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro Val Lys Ile Ala
 120 125 130

tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac 547
 Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His
 135 140 145

30 att ctg gat aag gtt gtg att gaa cga gtg aag aat gct ctc tcc cct 595
 Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro
 150 155 160 165

aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat 643
 Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His
 170 175 180

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta 691
 Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu
 185 190 195

40 cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta 739
 Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu
 200 205 210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat 787
 Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp
 215 220 225

50 gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac 835
 Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp
 230 235 240 245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa 883
 His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys
 250 255 260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta 935
 Val Leu Val Lys
 265

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<212> DNA

10 <213> Chlamydia pneumoniae

<220>

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<222> (101)..(385)

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 Met Leu Ala Phe Phe
 1 5

gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta 163
 Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu
 10 15 20

21 tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata 211
 Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile
 25 30 35

30 gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa 259
 Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu
 40 45 50

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta 307
 Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu
 55 60 65

40 atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt 355
 Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly
 70 75 80 85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct 405
 Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
 90 95

ctctaccaga gcttttttcc aacctaggtt ctgcttactt agattatatac tttcaacatc 465
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50 <210> 14

<211> 552

<212> PRT

<213> Chlamydia pneumoniae

<400> 14

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 Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu
 35 40 45
 Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile
 50 55 60
 10 Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr
 65 70 75 80
 Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu
 85 90 95
 Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu
 100 105 110
 20 Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala
 115 120 125
 Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln
 130 135 140
 Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala
 145 150 155 160
 Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe
 165 170 175
 30 Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu
 180 185 190
 Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe
 195 200 205
 Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met
 210 215 220
 40 Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys
 225 230 235 240
 Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu
 245 250 255
 Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly
 260 265 270
 Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala
 275 280 285
 50 Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser
 290 295 300
 Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys
 305 310 315 320

Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala
 325 330 335
 Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val
 340 345 350
 Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala
 355 360 365
 10 Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr
 370 375 380
 Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr
 385 390 395 400
 Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala
 405 410 415
 20 Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His
 420 425 430
 Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu
 435 440 445
 Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp
 450 455 460
 Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val
 465 470 475 480
 30 Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr
 485 490 495
 Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly
 500 505 510
 Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu
 515 520 525
 40 Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met
 530 535 540
 Val Arg Lys Glu Asn Arg Ser Lys
 545 550
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 <213> Chlamydia pneumoniae
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 Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly
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Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val
35 40 45

Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg
50 55 60

Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val
65 70 75 80

10 Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe
85 90 95

His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala
100 105 110

Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala
115 120 125

20 Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu
130 135 140

Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe
145 150 155 160

Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val
165 170 175

Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys
180 185 190

30 Ile Ala Arg Val
195

<210> 16

<211> 245

<212> PRT

<213> Chlamydia pneumoniae

<400> 16

40 Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser
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Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly
20 25 30

Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu
35 40 45

50 Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys
50 55 60

Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly
65 70 75 80

Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val
85 90 95

Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly
100 105 110

Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu
115 120 125

Val Gly Leu Ser Asp Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly
130 135 140

10 Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro
145 150 155 160

Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn
165 170 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr
180 185 190

20 Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn
195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe
210 215 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe
225 230 235 240

Ser Cys Ser Pro His
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<210> 17
<211> 278
<212> PRT
<213> Chlamydia pneumoniae

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Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe
35 40 45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu
50 55 60

50 Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg
65 70 75 80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln
85 90 95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys
100 105 110

B

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro
 115 120 125
 Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys
 130 135 140
 Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu
 145 150 155 160
 10 Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser
 165 170 175
 Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr
 180 185 190
 Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser
 195 200 205
 20 His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile
 210 215 220
 Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg
 225 230 235 240
 Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn
 245 250 255
 Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala
 260 265 270
 30 Thr Thr Phe Ser Ser Leu
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 <211> 469
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 <213> Chlamydia pneumoniae
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 20 25 30
 Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg
 35 40 45
 50 Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr
 50 55 60
 Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu
 65 70 75 80
 Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala
 85 90 95

Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys
 100 105 110
 Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys
 115 120 125
 Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile
 130 135 140
 10 Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn
 145 150 155 160
 Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn
 165 170 175
 Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile
 180 185 190
 20 Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr
 195 200 205
 Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln
 210 215 220
 Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu
 225 230 235 240
 Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser
 245 250 255
 30 Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile
 260 265 270
 Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met
 275 280 285
 Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met
 290 295 300
 40 Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val
 305 310 315 320
 Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr
 325 330 335
 Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu
 340 345 350
 50 Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala
 355 360 365
 Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile
 370 375 380
 Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg
 385 390 395 400

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly
405 410 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val
420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr
435 440 445

10 Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly
450 455 460

Ile Arg Phe Val Phe
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<210> 19

<211> 922

<212> PRT

<213> Chlamydia pneumoniae

20

<400> 19

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu
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Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
35 40 45

30

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
85 90 95

40 Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
130 135 140

50 Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
165 170 175

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
180 185 190

B

Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
 195 200 205
 Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
 210 215 220
 Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
 225 230 235 240
 10 Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
 245 250 255
 Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
 260 265 270
 Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
 275 280 285
 20 Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
 290 295 300
 Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
 305 310 315 320
 Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
 325 330 335
 Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
 340 345 350
 30 Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
 355 360 365
 Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr
 370 375 380
 Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
 385 390 395 400
 40 Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
 405 410 415
 Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
 420 425 430
 Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
 435 440 445
 Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
 450 455 460
 50 Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala
 465 470 475 480
 Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys
 485 490 495

Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu
500 505 510

Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser
515 520 525

Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
530 535 540

10 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
545 550 555 560

Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
565 570 575

Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
580 585 590

20 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg
595 600 605

Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
610 615 620

Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
625 630 635 640

Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
645 650 655

30 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
660 665 670

Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
675 680 685

Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
690 695 700

40 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
705 710 715 720

Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
725 730 735

Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
740 745 750

50 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
755 760 765

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
770 775 780

Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
785 790 795 800

His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
805 810 815

Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
835 840 845

10 Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
850 855 860

Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
865 870 875 880

Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
885 890 895

20 Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
915 920

<210> 20

<211> 375

<212> PRT

<213> Chlamydia pneumoniae

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20 25 30

Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr
35 40 45

40 Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser
50 55 60

Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly
65 70 75 80

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly
85 90 95

50 Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr
100 105 110

Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr
115 120 125

Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile
130 135 140

Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser
 145 150 155 160
 Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly
 165 170 175
 Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr
 180 185 190
 10 Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp
 195 200 205
 Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly
 210 215 220
 Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile
 225 230 235 240
 20 Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly
 245 250 255
 Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu
 260 265 270
 Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr
 275 280 285
 Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala
 290 295 300
 30 Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala
 305 310 315 320
 Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn
 325 330 335
 Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala
 340 345 350
 40 Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro
 355 360 365
 Lys Lys Gln Leu Leu Lys Ser
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 Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
 20 25 30

Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala
 340 345 350
 Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser
 355 360 365
 Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys
 370 375 380
 10 Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn
 385 390 395 400
 Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser
 405 410 415
 Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp
 420 425 430
 20 Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln
 435 440 445
 Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile
 450 455 460
 Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp
 465 470 475 480
 Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu
 485 490 495
 30 Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn
 500 505 510
 Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu
 515 520 525
 Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro
 530 535 540
 40 Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser
 545 550 555 560
 Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu
 565 570 575
 Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly
 580 585 590
 50 Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu
 595 600 605
 Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr
 610 615 620
 Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe
 625 630 635 640

Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn
 645 650 655
 Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala
 660 665 670
 Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala
 675 680 685
 10 Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr
 690 695 700
 Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg
 705 710 715 720
 Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu
 725 730 735
 20 Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile
 740 745 750
 Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr
 755 760 765
 Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly
 770 775 780
 Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn
 785 790 795 800
 30 Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala
 805 810 815
 Arg Gly Lys Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr
 820 825 830
 Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile
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 40 Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro
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 Gln Pro Lys Asn Gly Pro Ile
 865 870
 <210> 22
 <211> 963
 <212> PRT
 <213> Chlamydia pneumoniae
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 Phe Val Ser Ala Phe Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly
 20 25 30

Asn Glu Val Pro Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile
 35 40 45
 Ser Ala Phe His Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu
 50 55 60
 Pro Leu Val Ser Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly
 65 70 75 80
 10 His Asp Ile Thr Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser
 85 90 95
 Val Ile Asp Tyr Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys
 100 105 110
 Lys Asn Leu Phe Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg
 115 120 125
 20 Asn Ser Ser His Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys
 130 135 140
 Trp Ile Ser Lys Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser
 145 150 155 160
 Leu Ala Thr Thr Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu
 165 170 175
 Asp Ser Tyr Ile Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn
 180 185 190
 30 Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser
 195 200 205
 Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu
 210 215 220
 Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile
 225 230 235 240
 40 Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln
 245 250 255
 Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys
 260 265 270
 Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala
 275 280 285
 50 Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu
 290 295 300
 Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala
 305 310 315 320
 Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile
 325 330 335

Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala
 340 345 350
 Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu
 355 360 365
 Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Thr Ile Thr Ser
 370 375 380
 10 Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly
 385 390 395 400
 Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr
 405 410 415
 Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn
 420 425 430
 20 Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val
 435 440 445
 Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn
 450 455 460
 Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala
 465 470 475 480
 Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly
 485 490 495
 30 Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe
 500 505 510
 Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser
 515 520 525
 Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser
 530 535 540
 40 Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu
 545 550 555 560
 Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro
 565 570 575
 Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys
 580 585 590
 50 Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His
 595 600 605
 Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr
 610 615 620
 Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln
 625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg
 645 650 655
 His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala
 660 665 670
 Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp
 675 680 685
 10 Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn
 690 695 700
 Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala
 705 710 715 720
 Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe
 725 730 735
 20 Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr
 740 745 750
 Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe
 755 760 765
 Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp
 770 775 780
 His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys
 785 790 795 800
 30 Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe
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 Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser
 820 825 830
 Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp
 835 840 845
 40 His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser
 850 855 860
 Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met
 865 870 875 880
 Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn
 885 890 895
 50 Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr
 900 905 910
 Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn
 915 920 925
 Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala
 930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His
 945 950 955 960

Cys Thr Phe

<210> 23

<211> 514

<212> PRT

<213> Chlamydia pneumoniae

10

<400> 23

Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala
 1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr
 20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr
 35 40 45

20

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn
 50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly
 65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu
 85 90 95

30

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr
 100 105 110

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro
 115 120 125

Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met
 130 135 140

40

Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp
 145 150 155 160

Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser
 165 170 175

Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp
 180 185 190

Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr
 195 200 205

50

Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His
 210 215 220

Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser
 225 230 235 240

Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr
 245 250 255

B

Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser
260 265 270

Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr
275 280 285

Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu
290 295 300

10 Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser
305 310 315 320

Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu
325 330 335

Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser
340 345 350

20 Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala
355 360 365

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
370 375 380

Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
385 390 395 400

Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
405 410 415

30 Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
450 455 460

40 Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
500 505 510

50 Thr Pro

<210> 24
<211> 289
<212> PRT
<213> Chlamydia pneumoniae

<400> 24
Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr
1 5 10 15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe
 20 25 30
 Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe
 35 40 45
 Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu
 50 55 60
 10 Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile
 65 70 75 80
 Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu
 85 90 95
 Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr
 100 105 110
 20 Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln
 115 120 125
 Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro
 130 135 140
 His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val
 145 150 155 160
 Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val
 165 170 175
 30 Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala
 180 185 190
 Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met
 195 200 205
 Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp
 210 215 220
 40 Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile
 225 230 235 240
 Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr
 245 250 255
 Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala
 260 265 270
 50 Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val
 275 280 285

Leu

<210> 25

<211> 265

<212> PRT

<213> Chlamydia pneumoniae

<400> 25

Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn
 1 5 10 15

Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu
 20 25 30

Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr
 35 40 45

10

Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala
 50 55 60

Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly
 65 70 75 80

Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu
 85 90 95

20

Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu
 100 105 110

Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly
 115 120 125

Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala
 130 135 140

30

Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys
 145 150 155 160

Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser
 165 170 175

His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr
 180 185 190

Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe
 195 200 205

40

Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe
 210 215 220

Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu
 225 230 235 240

Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu
 245 250 255

50

Glu Gln Cys Met Lys Val Leu Val Lys
 260 265

<210> 26

<211> 95

<212> PRT

<213> Chlamydia pneumoniae

<400> 26

Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr
 1 5 10 15

Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile
 20 25 30

Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala
 35 40 45

10

Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val
 50 55 60

Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile
 65 70 75 80

Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
 85 90 95

20

<210> 27

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:14

<400> 27

Val Leu Phe Ile Ala His Phe Phe Leu
 5

30

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:14

40

<400> 28

Arg Ile Arg Glu Asp Arg Gln Ala Asn
 5

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

50

<223> T-cell epitope from SEQ ID NO:15

<400> 29

Lys Leu Met Val Phe Gln Lys Trp Ala
 5

<210> 30

<211> 11

<212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:15

<400> 30
 Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr
 5 10

10

<210> 31
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T-cell epitope from SEQ ID NO:16

<400> 31
 Tyr Met Asn Lys Thr Leu His Phe Ile
 5

20

<210> 32
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:16

30

<400> 32
 Ser Trp His Gly Lys Tyr Lys Lys Lys Asp Phe Glu
 5 10

<210> 33
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:16

40

<400> 33
 Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn Gln Gln Arg
 5 10

<210> 34
 <211> 9
 <212> PRT
 <213> Artificial Sequence

50

<220>
 <223> T-cell epitope from SEQ ID NO:17

<400> 34
 Trp Leu Ser Pro Lys Asn Leu Lys Val
 5

<210> 35
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:17

<400> 35
 10 Asn His Tyr Asp Pro His Thr Tyr Glu Leu Pro Pro Gln Gln Ile Lys
 5 10 15

Glu Leu Arg Gln Gly Asp
 20

<210> 36
 <211> 9
 <212> PRT
 <213> Artificial Sequence

20 <220>
 <223> T-cell epitope from SEQ ID NO:18

<400> 36
 Trp Leu Phe Asp Leu Arg Phe Ser Val
 5

<210> 37
 <211> 18
 <212> PRT
 <213> Artificial Sequence

30 <220>
 <223> B-cell epitope from SEQ ID NO:18

<400> 37
 Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His
 5 10 15

40 Ser Thr

<210> 38
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T-cell epitope from SEQ ID NO:19

50 <400> 38
 Ala Leu Met Leu Leu Asn Asn Tyr Val
 5

<210> 39
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:19

<400> 39

Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly
 5 10

<210> 40

<211> 9

10 <212> PRT

<213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:20

<400> 40

Val Leu Phe Gln Asp Asn Ser Ala Leu
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20 <210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:20

<400> 41

Asn Ser Ser Lys His Asp Gly
 5

30

<210> 42

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:21

40 <400> 42

Trp Leu Leu Thr Ser Ser Ala Leu Val
 5

<210> 43

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

50 <223> B-cell epitope from SEQ ID NO:21

<400> 43

Gln Lys Asn Thr Ser Glu Lys Asp Gly
 5

<210> 44

<211> 16

<212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:21

<400> 44
 Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala Asn Gln Glu Gly
 5 10 15

10

<210> 45
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T-cell epitope from SEQ ID NO:22

<400> 45
 20 Gln Leu Tyr Val Asp Trp Thr Pro Val
 5

<210> 46
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:22

30

<400> 46
 Asn Gln His Asn Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr
 5 10 15

Gly

<210> 47
 <211> 17
 <212> PRT
 40 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:22

<400> 47
 Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn
 5 10 15

Tyr

50

<210> 48
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> B-cell epitope from SEQ ID NO:23

<400> 48

Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro
 5 10 15

Thr Lys Lys

<210> 49

<211> 9

<212> PRT

10 <213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:24

<400> 49

Tyr Met Asp Asn Asn Leu Phe Tyr Val
 5

<210> 50

20 <211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:24

<400> 50

Thr Gln Ile Thr Asn Tyr Met Asp Asn Asn
 5 10

30

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:25

<400> 51

40 Phe Leu Trp Tyr Phe Leu Arg Arg Leu
 5

<210> 52

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:25

50

<400> 52

Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg
 5 10

<210> 53

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> T-cell epitope from SEQ ID NO:26

<400> 53

Leu Leu Leu Ile Leu Ile Val Ser Ala

5

<210> 54

<211> 7

10 <212> PRT

<213> Artificial Sequence

<220>

<223> B-cell epitope from SEQ ID NO:26

<400> 54

Gln Asn Phe Tyr Lys Trp Lys

5





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Figure 14: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 14; ORF: cpn100686

```
1  MVSSPILNVP LKNHASVSGK FTHREVSKLA SDLKSGAMSF VPEVLSEETI
51 SSDLGKKQCT QGIISACCGL AMLIVLMSVY YRFGGVIASG AVLLNLLLIW
101 AALQYLDAPL TLSGLAGIVL AMGMAVDANV LVFERIREEF LLSQSLKKS
151 EKGYTKAFGA IFDSNLTTVL ASALLFFLDT GPIKGFALT ILGIFSSMFT
201 ALFMTKFFFM LWMNKTQHTQ LHMMNKFVGI KHDFLRGCKK LWAVSGSVFL
251 LGCVALGFGA WNSVLGMDFK GGYAFTFNP EHGSDVAQM RGKVVHKLQE
301 AGLSSRD FRI QTFGSSEKIK IYFSDKALSY TKQIRASLLK LTIMSWRYCG
351 IVVRNRPRFL YGNSKRNAKF WSKVSSKLSK KMRVQATIGL LGALAIILLY
401 VSLRFEWQYA FSAVCALIHD LLATCAVLFI AHFFLKKIQI DLQAIGALMT
451 VLGYSLNNTL IIFDRIREDR QANLFTPMHV LVNDALQKTF SRTVMTTATT
501 LSVLLMLLFI GGSSVFNFAP IMTIGILLGT LSSLYIAPPL LLFMVRKENR
551 SK
```

Possible T cell epitope:

427 VLFIAHFFL (SEQ ID NO: 27)

Possible B cell epitope:

465 RIREDRQAN (SEQ ID NO: 28)

Figure 15: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 15; ORF: cpn100696

1 MSSNLHPVGG TGTGAAAPES VLNIVEEIAA SGSVTAGLQA ITSSPGMVNL
51 LIGWAKTKFI QPIRESKLFQ SRACQITLLV LGILLVVAGL ACMFIFHSQL
101 GANAFWLIIP AAIGLIKLLV TSLCFDEACT SEKLMVFQKW AGVLEDQLDD
151 GILNNSNKIF GHVKTEGNTS RATTPVLNDG RGTPVLSPLV SKIARV

Possible T cell epitope:

133 KLMVFQKWA (SEQ ID NO: 29)

Possible B cell epitope:

163: VKTEGNTSRAT (SEQ ID NO: 30)

Figure 16: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 16; ORF: cpn100709

```

  1 MTIRILAEGL AFRYGSKGPN IIHDVSFSVY DGDFIGIIGP NGGKSTLTM
 51 LILGLLTPTF GSLKTFPSHS AGKQTHSMIG WVPQHFSYDP CFPISVKDVV
101 LSGRLSQLSW HGKYKKKDFE AVDHALLDLVG LSDTTTTAFA HLSGGQIQRV
151 LLARALASYP EILILDEPTT NIDPDNQQRI LSILKKLNRT CTILMVTHDL
201 HHTTNYFNKV FYMNKTLHFI GRHFDLNRPI LLSSYKNQEF SCSPH

```

Possible T cell epitope:

212 YMNKTLHFI (SEQ ID NO: 31)

Possible B cell epitopes:

109 SWHGKYKKKDFE (SEQ ID NO: 32)

166 DEPTTNIDPDNQQR (SEQ ID NO: 33)

Figure 17: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 17; ORF: cpn100710

1 MHKVIVFIFL TLYSLKSYGN DVIDKPHVLV SIAPYKFLVE QIAEETCFVY
51 AIVTNHYDPH TYELPPQQIK ELRQGDWFR IGEAFGKNLL EKPVMQQVDL
101 SQNVSLIQGK PCCNQHTTNY DTHTWLS PKN LKVQVETIVT TLSKKYPQHA
151 TLYQSNGEKL LLALDQLNEE ILTITSKAKQ RHILVSHGAF GYFCRDYNFS
201 QHTIEKSSHV EPSPKDVARV FRDIEQYKIS SVILLEYSGR RSSAMLADRF
251 HMHTVNLDPY AENVLVNLKT IATTFSSL

Possible T cell epitope:

125 WLSPKNLKV (SEQ ID NO: 34)

Possible B cell epitope:

55 NHYDPHTYELPPQQIKELRQGD (SEQ ID NO: 35)

Figure 18: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 18; ORF: cpn100711

1	MGPGSVLSNH	SKEAGGIAIN	NVIIDFSEIV	PTKDNATVAP	PTLKLVSRTN
51	ADSKDKIDIT	GTVTLLDPNG	NLYQNSYLGE	DRDITLFNID	NSASGAVTAT
101	NVTLQGNLGA	KKGYLGTWNL	DPNSSGSKI I	LKWTFDKYLR	WPYIPRDNHF
151	YINSIWGAQN	SLVTVNQGIL	GNMLNNARFE	DPAFNNFWAS	AIGSFLRKEV
201	SRNSDSFTYH	GRGYTAAVDA	KPRQEFILGA	AFSQVFGHAE	SEYHLDNYKH
251	KSGSHSTQAS	LYAGNIFYFP	AIRSRPILFQ	GVATYGYMQH	DTTTYYPsie
301	EKNMANWDSI	AWLFDLRFVS	DLKEQPQPHST	ARLTFYTEAE	YTRIRQKEFT
351	EKDYDPRSFS	ACSYGNLAIP	TGFSVDGALA	WREIILYNKV	SAAYLPVILR
401	NNPKATYEV L	STKEKGNVVN	VLPTRNAARA	EVSSQIYLGS	YWTLYGTYTI
451	DASMNTLVQM	ANGGIRFVF			

Possible T cell epitope:

312 WLFDLRFSV (SEQ ID NO: 36)

Possible B cell epitope:

240: ESEYHLDNYKHKSGHST` (SEQ ID NO: 37)

Figure 19: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 19; ORF: cpn100877

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1  MRFSLCGFPL VFSFTLLSVF DTSLSATTIS LTPEDSFHGD SQNAERSYNV
51 QAGDVYSLTG DVSISNVDNS ALNKACFNVT SGSVTFAGNH HGLYFNNISS
101 GTTKEGAVLC CQDPQATARF SGFSTLSFIQ SPGDIKEQGC LYSKNALMLL
151 NNYVVRFEQN QSKTKGGAIS GANVTIVGNY DSVSFYQNAA TFGGAIHSSG
201 PLQIAVNQAE IRFAQNTAKN GSGGALYSDG DIDIDQNAYV LFRENEALTT
251 AIGKGGAVCC LPTSGSSTPV PIVTFSDNKQ LVFERNHSIM GGGAIYARKL
301 SISSGGPTLF INNISYANSQ NLGGAIAIDT GGEISLSAEK GTITFQGNRT
351 SLPFLNGIHL LQNAKFLKLQ ARNGYSIEFY DPITSEADGS TQLNINGDPK
401 NKEYTGILF SGEKSLANDP RDFKSTIPQN VNLSAGYLV I KEGAEVTVSK
451 FTQSPGSHLV LDLGTKLIAS KEDIAITGLA IDIDSLSSSS TAAVIKANTA
501 NKQISVTD SI ELISPTGNAY EDLRMRNSQT FPLLSLEPGA GGSVTVTAGD
551 FLPVSPHYGF QGNWKLAWTG TGNKVGEFFW DKINYKPRPE KEGNLV PNIL
601 WGNVAVDVRSL MQVQETHASS LQTDRLWID GIGNFFHVSA SEDNIRYRHN
651 SGGYVLSVNN EITPKHYTSM AFSQLFSRDK DYAVSNNEYR MYLGSYLYQY
701 TTSLGNIFRY ASRNPVN NVG ILSRRFLQNP LMIFHFLCAY GHATNDMKTD
751 YANFPMVKNS WRNNCWAIEC GGSMPLLVFE NGRLFQGAIP FMKLQLVYAY
801 HGDFKETAD GRRFSNGSLT SISVPLGIRF EKLALSQDVL YDFSFSYIPD
851 IFRKDPSCEA ALVISGDSWL VPAAHVSRA FVGSGTGRYH FNDYTELLCR
901 GSIECRPHAR NYNINCGSKF RF

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Possible T cell epitope:

146 ALMLLN NYV (SEQ ID NO: 38)

Possible B cell epitope:

581 DKINYKPRPEKEG (SEQ ID NO: 39)

Figure 20: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 20; ORF: CPN100325

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1 MPSSWKRLQ VLSHKIAATE SGGGIYAKDI QLQALPGSFT ITDNKVETSL
51 TTSTNLYGGG IYSSGAVTLT NISGTFGITG NSVINTATSQ DADIQGGGIY
101 ATTSL SINQC NTPILFSNNS AATKKTSTTK QIAGGAIFSA AVTIENNSQP
151 IIFLNNSAKS EATTAATAGN KDSCGGAIAA NSVTLTNNPE ITFKGNYAET
201 GGAIGCIDLT NGSPPRKVS I ADNGSVLFQD NSALNRGGAI YGETIDISRT
251 GATFIGNSSK HDGSAICCST ALTLAPNSQL IFENNKVTET TATTKASINN
301 LGAAIYGNNE TSDVTISLSA ENGSIFFKNN LCTATNKYCS IAGNVKFTAI
351 EASAGKAISF YDAVNVPPKK QLLKS
```

Possible T cell epitope:

226 VLFQDNSAL (SEQ ID NO: 40)

Possible B cell epitope:

257 NSSKHDG (SEQ ID NO: 41)

Figure 21: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 21; ORF: CPN100368

Figure 22: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 22; ORF: CPN100624

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 1 MTNSIFISKF GCLCDPFVSA FYPTALCCSL SGNEVPNLAS CQMSRKDISA
51 FHTSPSFRLN VTPEPLVSSF RPSNLLNGFG HDITQDITIT GNSINSVIDY
101 NYHYEDGGIL ACKNLFISEN KGNLSFERN SSSGGALYS VRECWISKNQ
151 NYSFISNAAS LATTTTSGFG GAIHALDSYI TNNLGEGQFL DNVSKNRGGA
201 IYVGVSLSIT DNLGPIVIKK NQTLEDSSFG GGIFCRAVNI ERNYQNIQIN
251 DNASQGQVVY FLPLGVIISS NKEIIEISNH SASSINTASG KLYPGGGGIM
301 CTSLSHENNP KGLIFNNKTA ALSGGVYTRD LSSSKITVRT AFINNSATSG
351 GALINLSGIG STPQNFFLSA DYGDILFNNN TITSSSPQPG YRNALYAAPG
401 INLKLGARQG YKILFYDPID HDQTTTDPID FNYEPHHLGT VLFSGINVDS
451 NATNPLNFLS KFSNSSLRLER GVLAIEDRAA ISCKTLSQTG GILRLGNAAL
501 IRTKGPSSSI NFNAIAINLP SILQSEASAP KFWIYPTLTG STYSEDTSST
551 ITLSGPLTFL NDENENPYDS LDLSEPRKDI PPPLPPRCDC KKIDTSNLIV
601 EAMNLDEHYG YQGIWSPYWM ETTTTSSTV PEQNTNHRQ LYVDWTPVGY
651 RPNPERHGEF IANTLWQSAY NALLGIRILP PQNLKEHDLE ASLQGLGLLI
701 NQHNREGRKG FRNHTTGYYA TTSAKTAARH SFSLGFAQMF SKTRERQSPS
751 TTSSHNYFAG LRFDSLFLRD FISTGLSLGY SYGDHMLCH YTEILKGSSK
801 AFFNNHTLVA SLDCTFLPAR ITRTLELQPF ISAIALRCSQ ASFQETGDHI
851 RKFHFKHPLT DLSSPIGFRS EWKTSHHIPM LWTTEISYVP TLYRKNPEMF
901 TTLLISNGTW TTQATPVSYN SVAARIKNTS QLFSRVTLSL DYSAQVSSST
951 VGQYLKAESH CTF

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Possible T cell epitope:

640 QLYVDWTPV (SEQ ID NO: 45)

Possible B cell epitopes:

701 NQHNREGRKGFRNHTTG (SEQ ID NO: 46)

741 SKTRERQSPSTSSHNY (SEQ ID NO: 47)

Figure 23: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 23; ORF: CPN100633

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 1 MTILRNFLTC SALFLALPAA AQVVYLHESD GYNGAINNKS LEPKITCYPE
51 GTSYIFLDDV RISNVKHDQE DAGVFINRSG NLFFMGNRCN FTFHNLMTG
101 FGAAISNRVG DTTLTLSNFS YLAFTSAPLL PQQGAIYSL GSVMIENCEE
151 VTFCGNYSSW SGAAIYTPYL LGSKASRPSV NLSGNRYLVF RDNVSQVYGG
201 AISTHNLTLT TRGPSCFENN HAYHDVNSNG GAIAIAPGGS ISISVKSGDL
251 IFKGNTASQD GNTIHNSIHL QSGAQFKNLR AVESGVYFY DPISHSESHK
301 ITDLVINAPE GKETYEGTIS FSGLCLDDHE VCAENLTSTI LQDVTLAGGT
351 LSLSDGVTLQ LHSFKQEASS TLTMSPGTTL LCSGDARVQN LHILIEDTDN
401 FVPVRIRAED KDALVSLEKL KVAFEAYWSV YDFPQFKEAF TIPLLELLGP
451 SFDSL LLGET TLERTQVTTE NDAVRGFWSL SWEEYPPSLD KDRRITPTKK
501 TVFLTWNPEI TSTP

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~~Possible T cell epitope:~~

~~640 QLYVDWTPV~~

Possible B cell epitope:

482 WEEYPPSLDKDRRITPTKK

(SEQ ID NO: 48)

Figure 24: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 24; ORF: cpn100985

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  1 MGISLPELFS NLGSAYLDYI FQHPPAYVWS VFLLLLLARLL PIFAVAPFLG
 51 AKLFPSPIKI GISLSWLAIH FPKVLADTQI TNYMDNNLFY VLLVKEMIIG
101 IVIGFVLAFP FYAAQSAGSF ITNQGGIQGL EGATSLISIE QTSPHGILYH
151 YFVTIIFWLV GGHRIVISLL LQTLEVIPIH SFFPAEMMSL SAPIWITMIK
201 MCQLCLVMTI QLSAPAALAM LMSDLFLGII NRMAPQVQVI YLLSALKAFM
251 GLLFLTLAWW FIIKQIDYFT LAWFKEVPIM LLGSPNPQVL

```

Possible T cell epitope:

83 YMDNNLFYV (SEQ ID NO: 49)

Possible B cell epitope:

78 TQITNYMDNN (SEQ ID NO: 50)

Figure 25: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 25; ORF: cpn100987

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1 MKHSKEDDLS RFLPKNLLVE SPHP EEIPLK SLSFTMSWLP TIHPSWITIA
51 MKEFPPEIQG QLLAWLPEPL VQEILPLLPG ISIAPHRCAP FGAFYLLDML
101 SKKIRPCGIT EEIFLPASSA NAILYTGPV KIALINCLGL YSIAKELKHI
151 LDKVVIERVK NALSPTEKLF LTYCQSHPMK HLETTNFLSS WTTDAELRQF
201 VHKGLEFLG KALTKENASF LWYFLRRLDV GRAYIVEQTL KTWYDHPYVD
251 YFKSRLEQCM KVLVK
```

Possible T cell epitope:

220 FLWYFLRRL (SEQ ID NO: 51)

Possible B cell epitope:

1 MKHSKEDDLSR (SEQ ID NO: 52)

Figure 26: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 26; ORF: cpn100988

1 MLAFFATSFK SVLFEYSYQS LLLILIVSAP PIILASIVGI MVAIFQAATQ
51 IQEQTFFAFV KLVVIFGTLM ISGGWLSNMI LRFAGQIFQN FYKWK

Possible T cell epitope:

21 LLLILIVSA (SEQ ID NO: 53)

Possible B cell epitope:

89 QNFYKWK (SEQ ID NO: 54)